

1 MELAALCRWG LLLALLPPGA ASTQVCTGTD MKLRLPASPE THLDMLRHLY QGCQVQGNL LSFLODIQEV QGYVLIAHNQ VRQVPLQRLR
101 IVRGTQLFED NYALAVLDNG DPLNNTTPVT GASPGGLREL QLRSLTEILK GGVLIQRNPQ LCYQDTILWK DIFHKNNQLA LTLIDTNRSR ACHPCSPMCK
201 GSRGWGESSE DCQSLTRTVC AGGCARCKGP LPTDCCHEQC AAGCTGPKHS DCLACLHFNH SGICELHCPA LVTYNTDTFE SMPNPEGRYT FGASCVTACP
301 YNYLSTDVGS CTLVCPLHNQ EVTAEDGTQR CEKCSKPCAR VCYGLGMEHL REVRAVTSAN IQEFAGCKKI FGSIAFLPES FDGDPASNTA PLQPEQLQVF
401 ETLEETGYL YISAWPDSLP DLSVFQNLQV IRGRILHNGA YSLTLQGLGI SWLGLSLRE LGSGLALIH NTHLCFVHTV PWDQLFRNPQ QALLHTANRP
501 EDECVGEGLA CHQLCARGHC WGPPTQCVN CSQFLRGQEC VEECRVLQGL PREYVNAHRC LPCHPECPQ NGSVTCFGPE ADQCACAHY KDPPFCVARC
601 PSGVKPDLSY MPIWKFPDEE GACQPCPINC THSCVDLDDK GCPAE (SEQ ID NO: 13)

FIG. 1A

| | | | |
|------|----|---------|----------------|
| 7C2 | aa | 22-53 | (31 RESIDUES) |
| 7F3 | aa | 22-53 | (31 RESIDUES) |
| 2C4 | aa | 22-584 | (562 RESIDUES) |
| 7D3 | aa | 22-584 | (562 RESIDUES) |
| 3E8 | aa | 512-625 | (113 RESIDUES) |
| 4D5 | aa | 529-625 | (96 RESIDUES) |
| 2H11 | aa | 529-645 | (116 RESIDUES) |
| 3H4 | aa | 541-599 | (58 RESIDUES) |

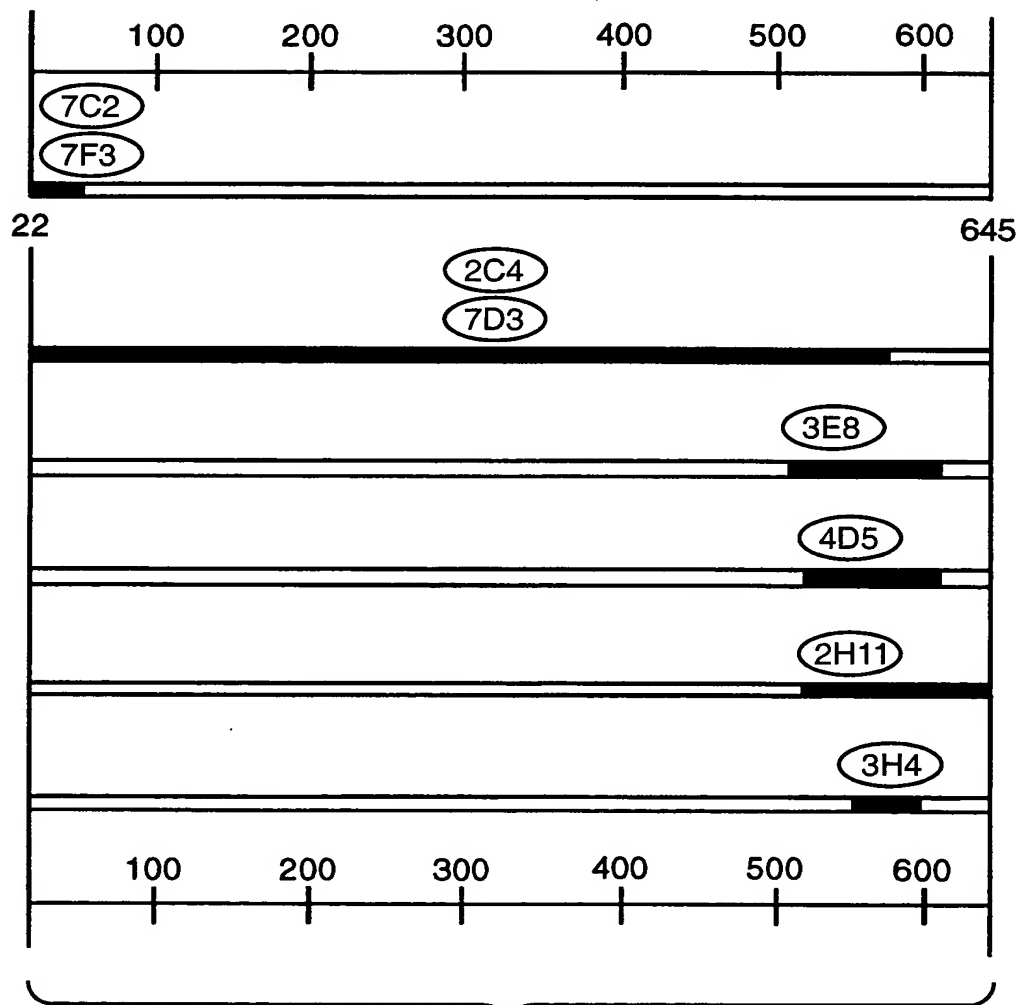


FIG. 1B

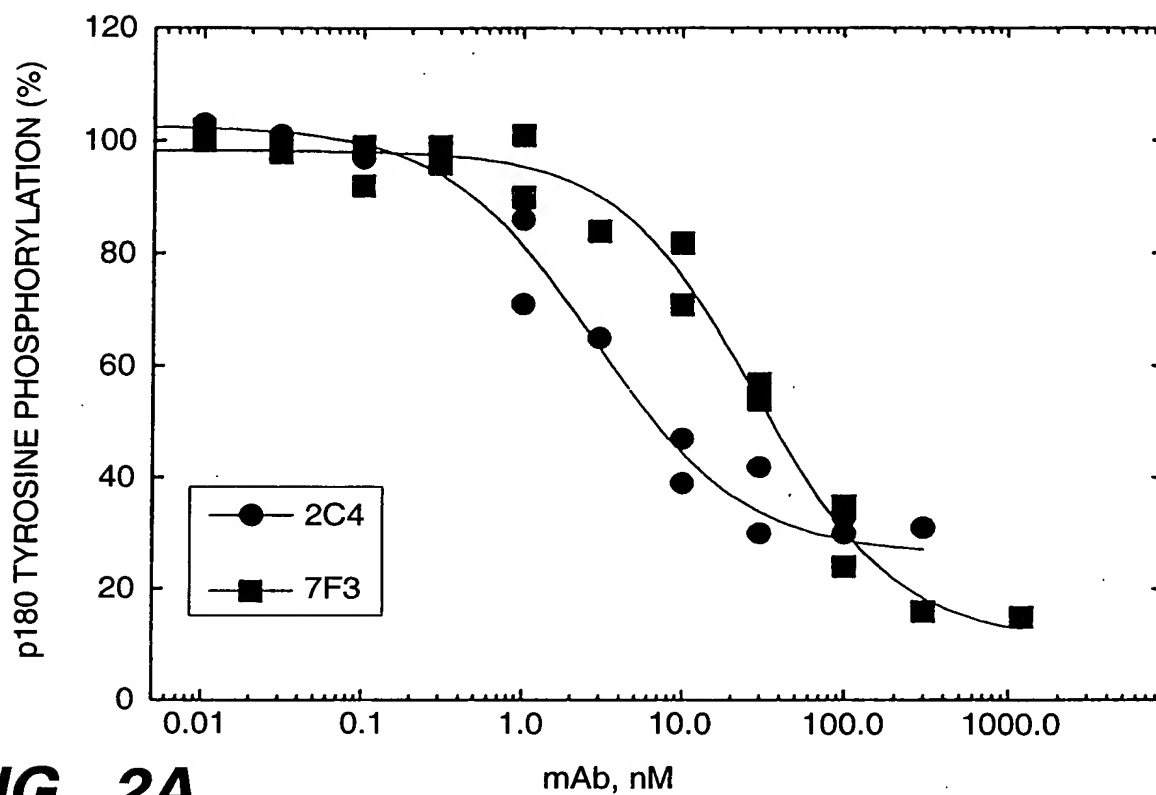


FIG. 2A

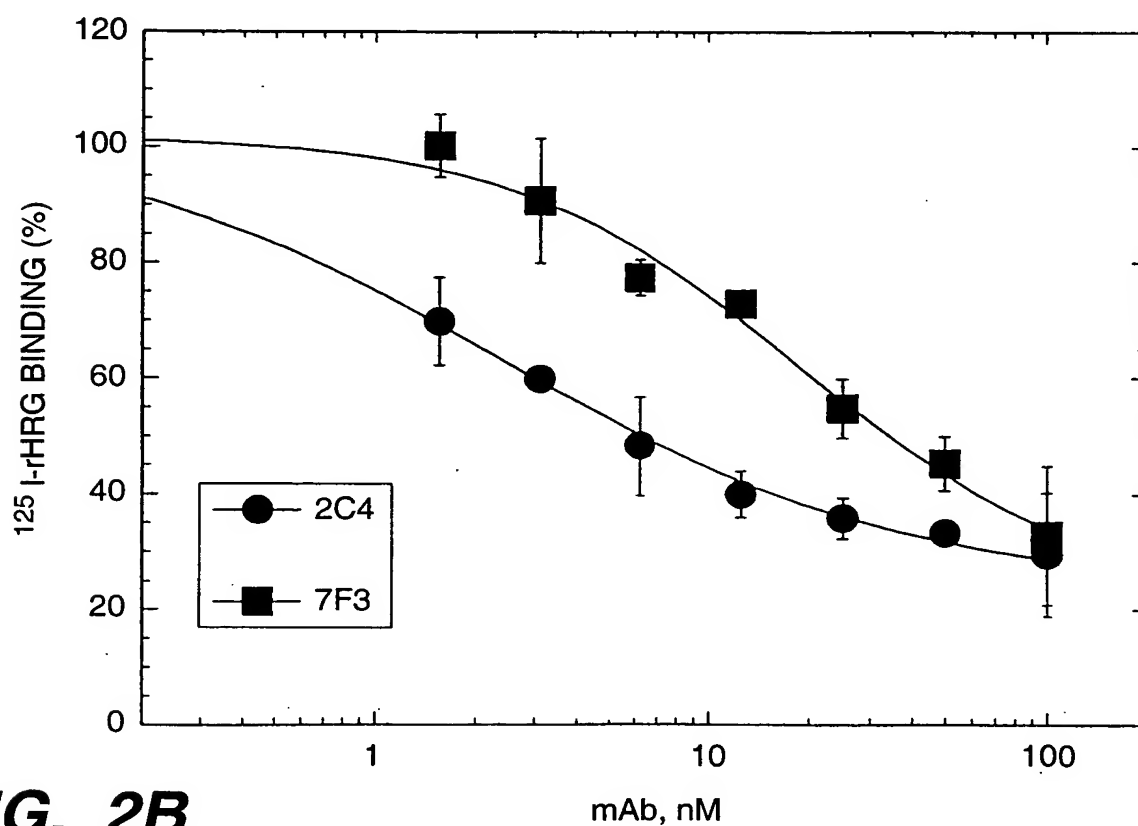


FIG. 2B

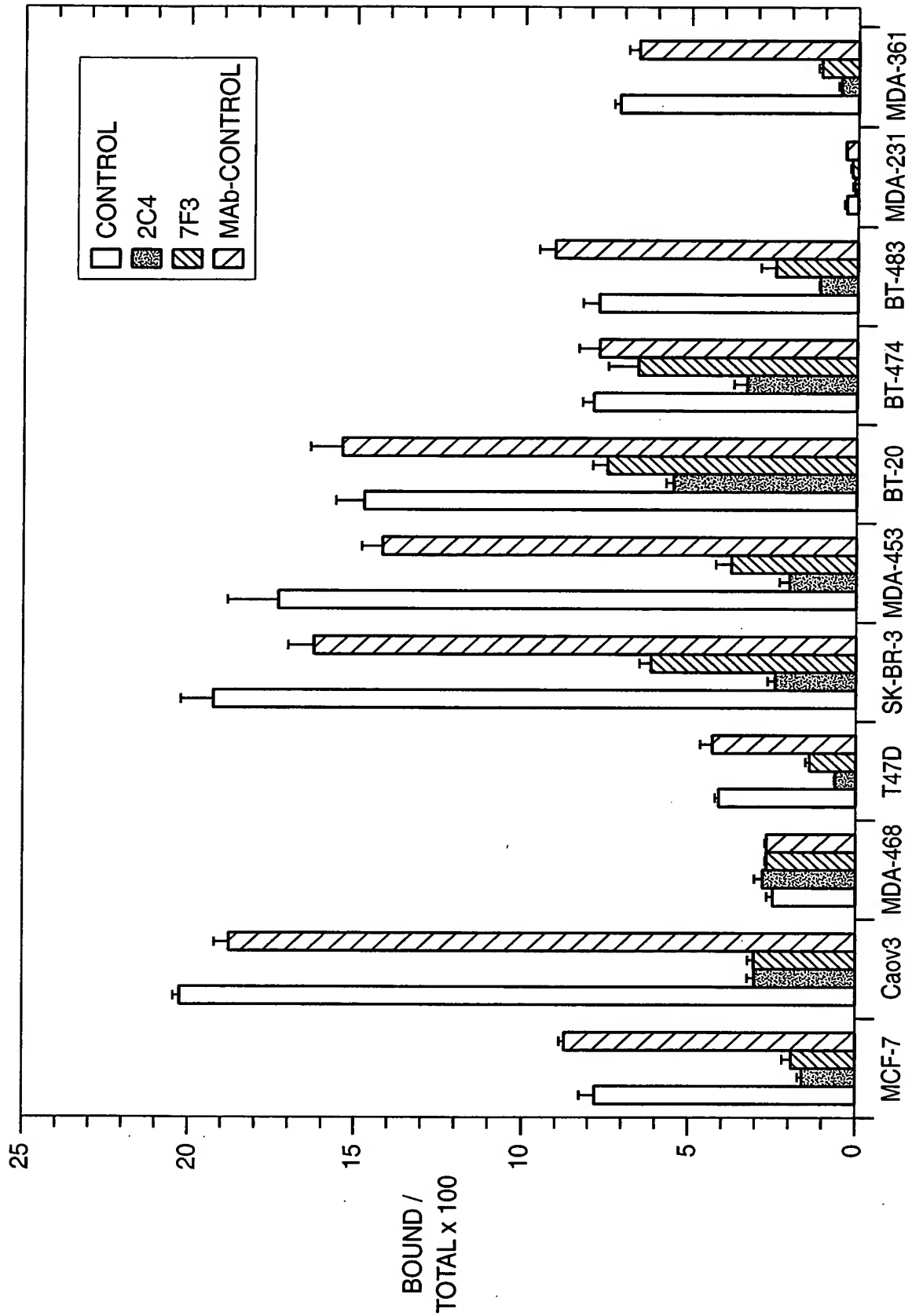


FIG. 3

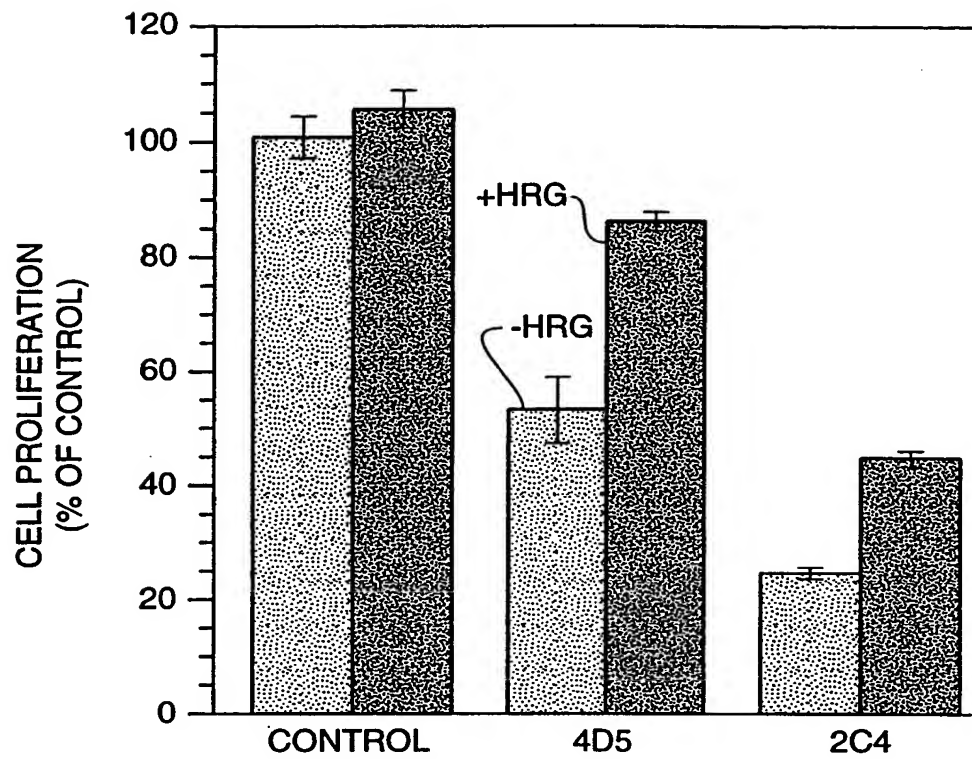


FIG. 4A

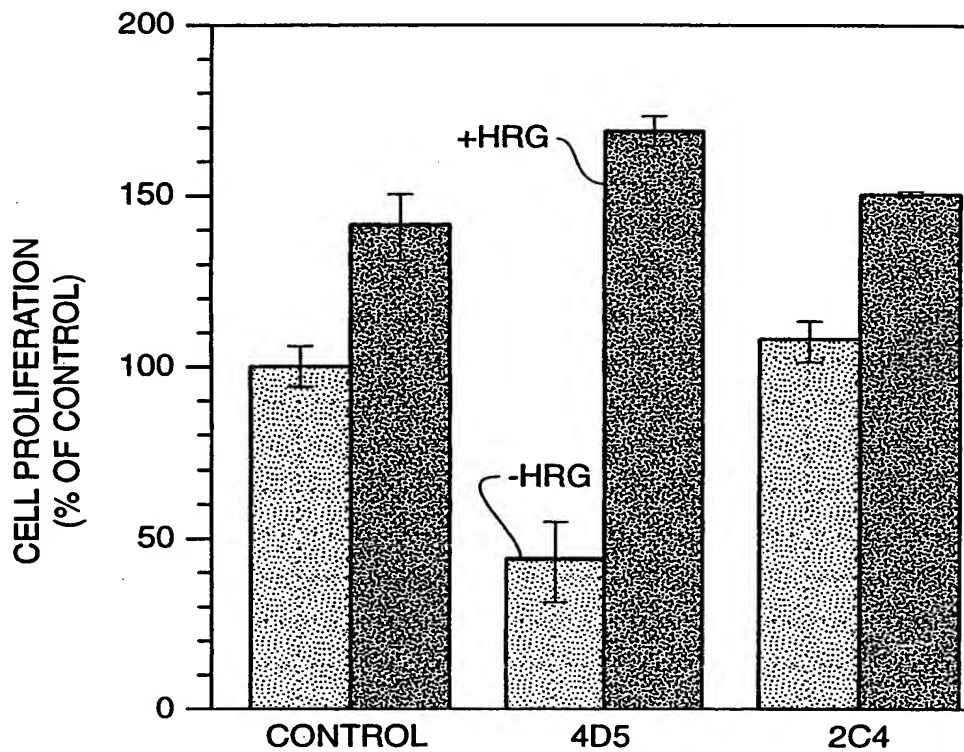
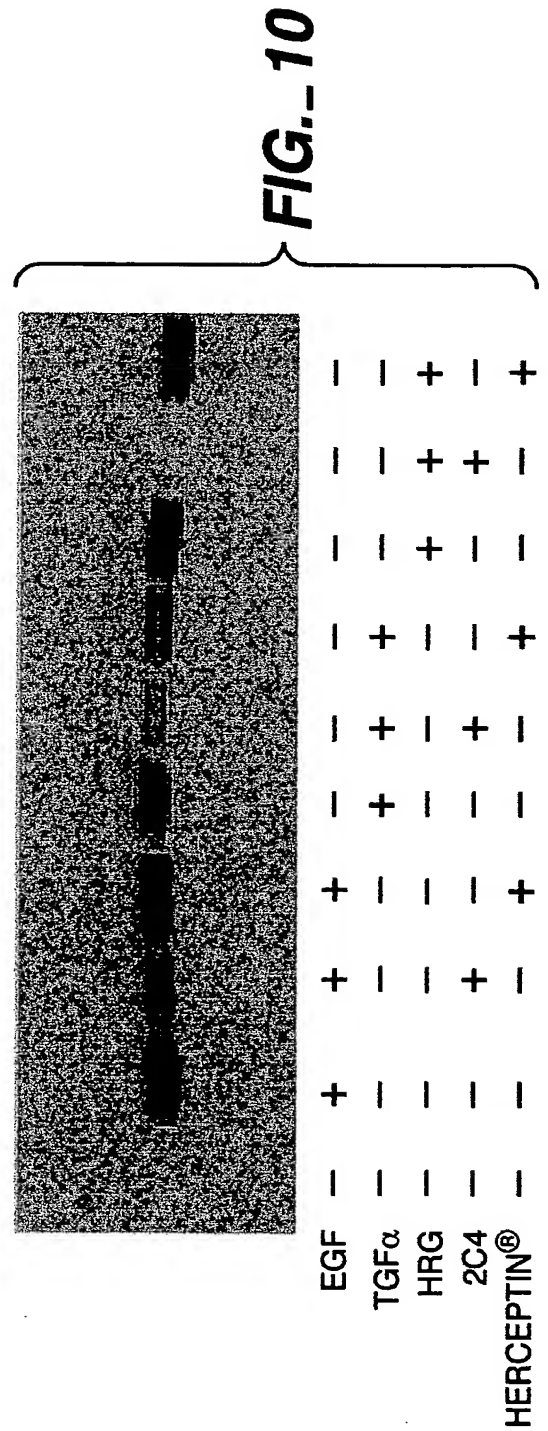
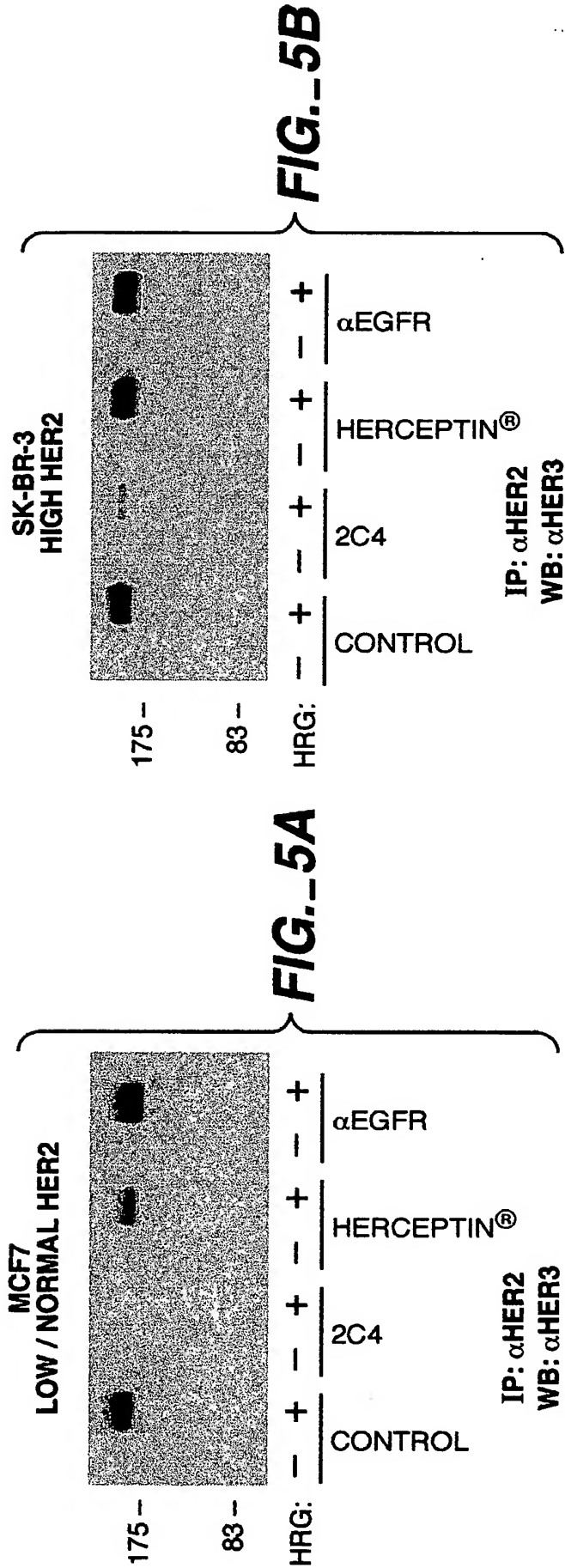


FIG. 4B



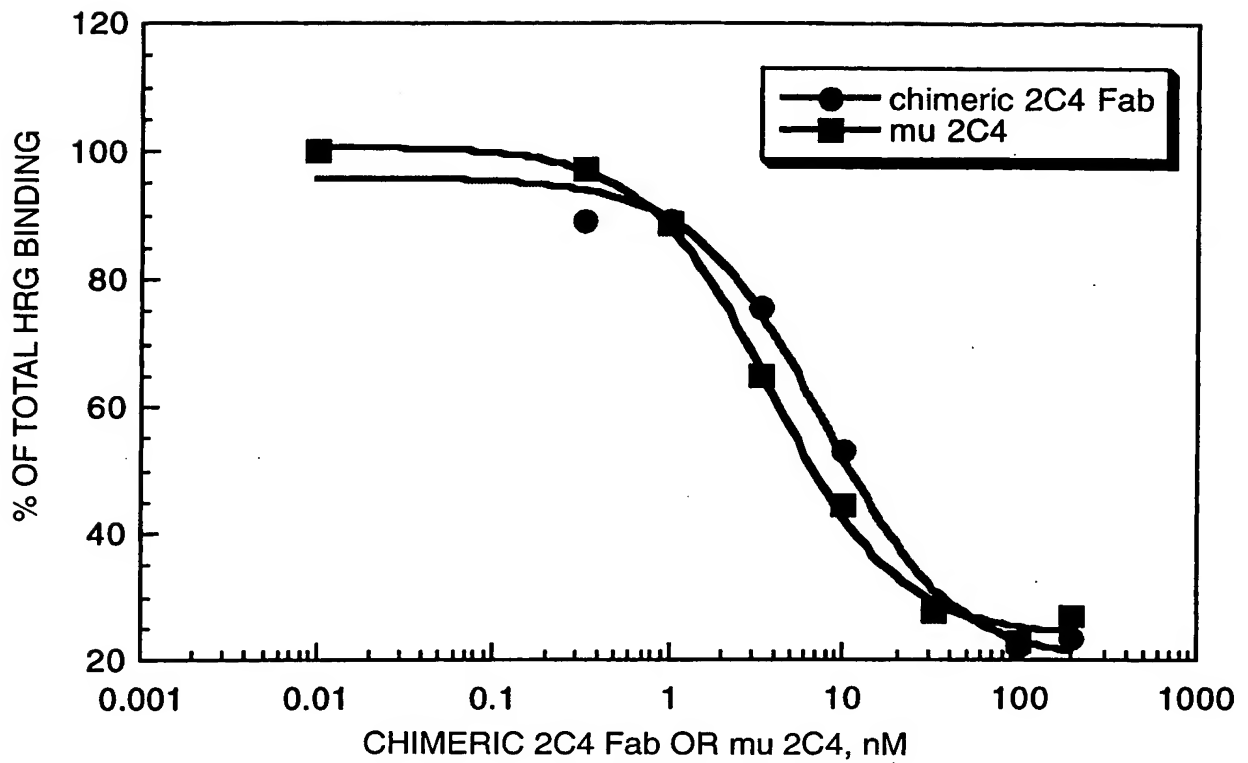


FIG._6A

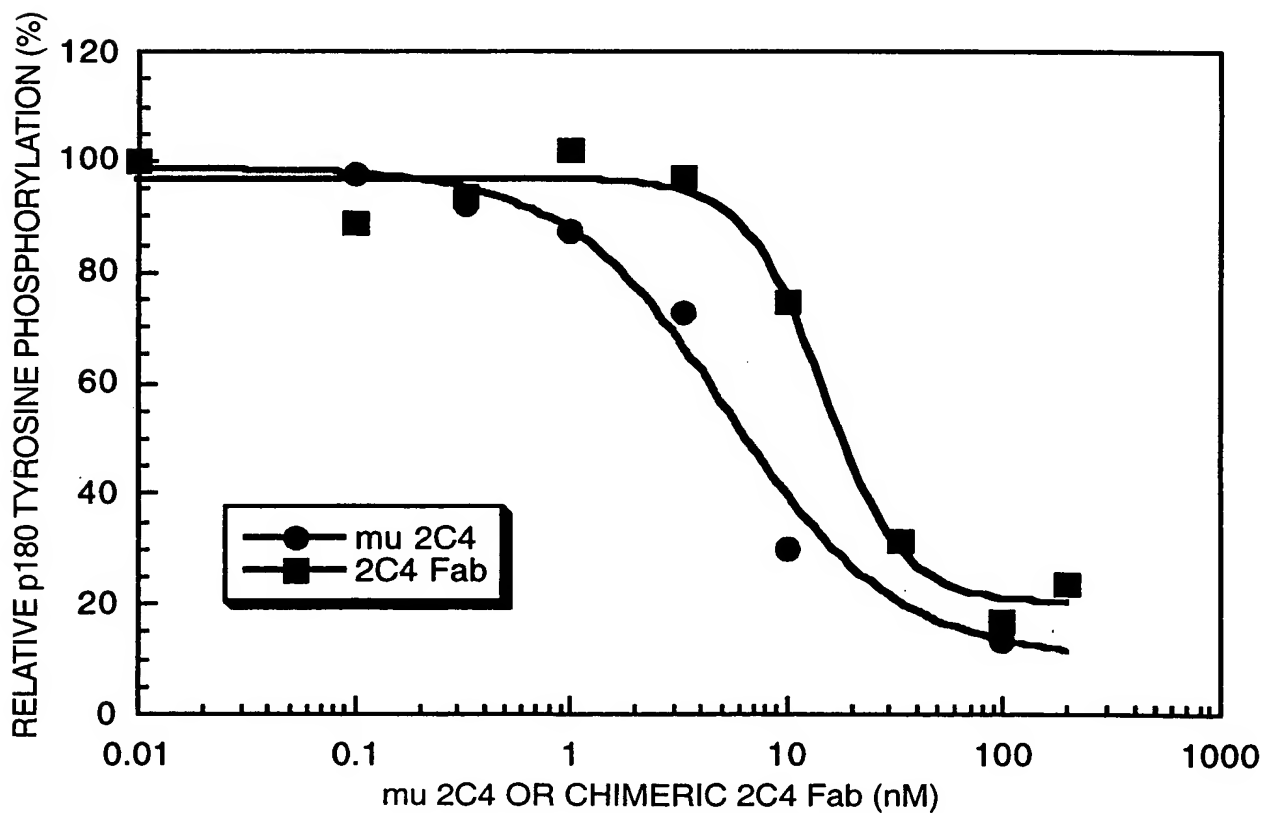


FIG._6B

FIG. 7B

+

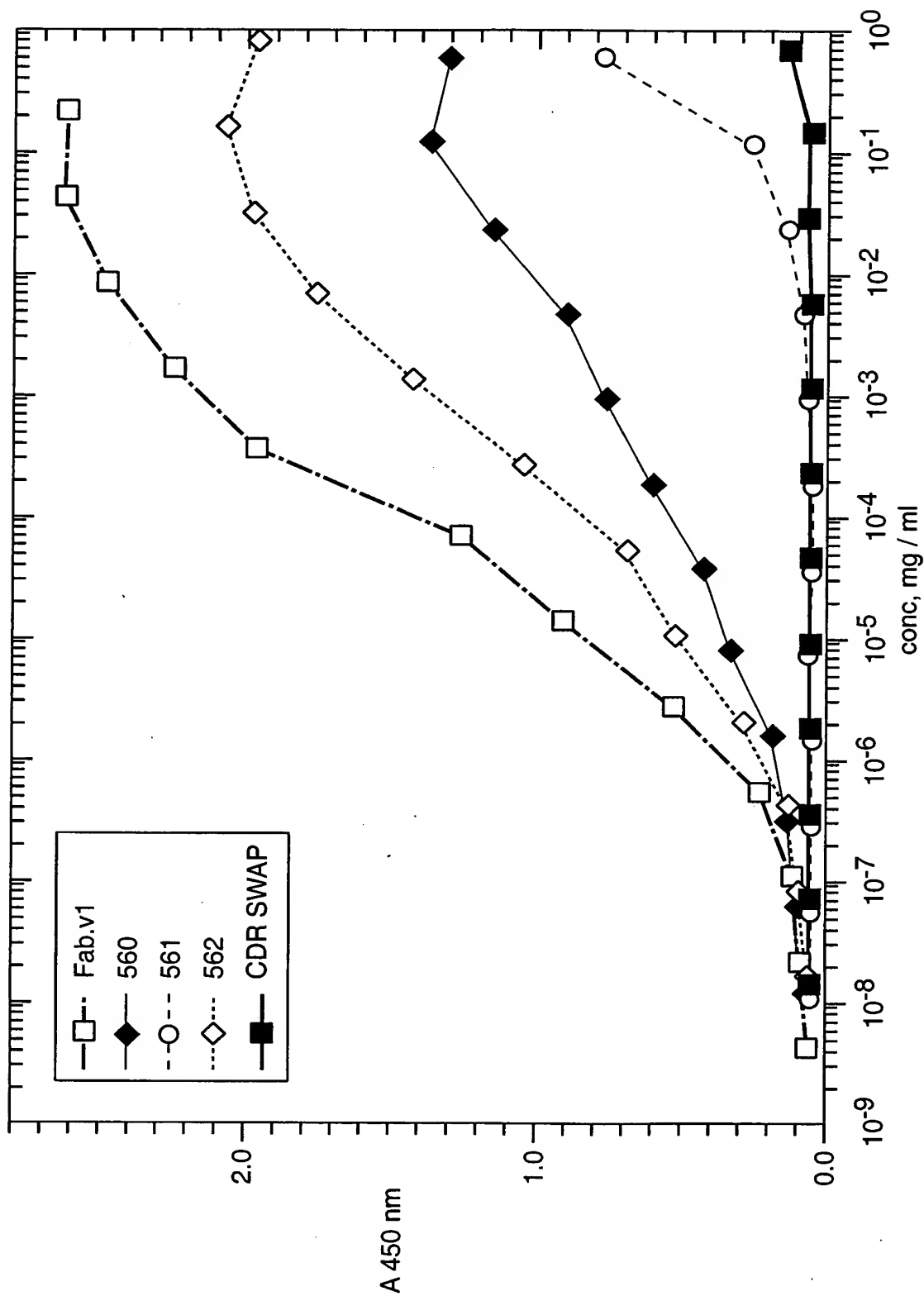


FIG._8A

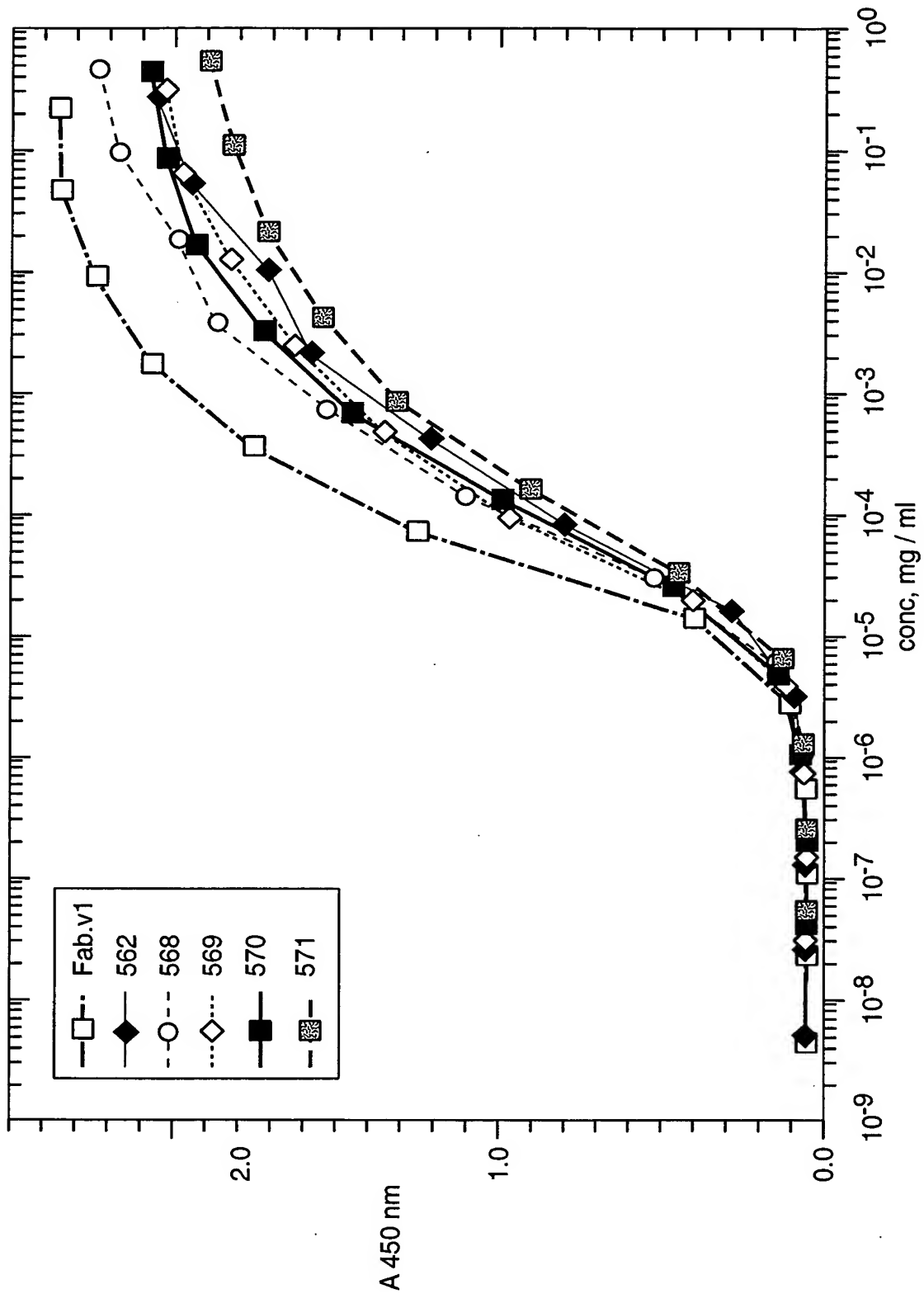


FIG._8B

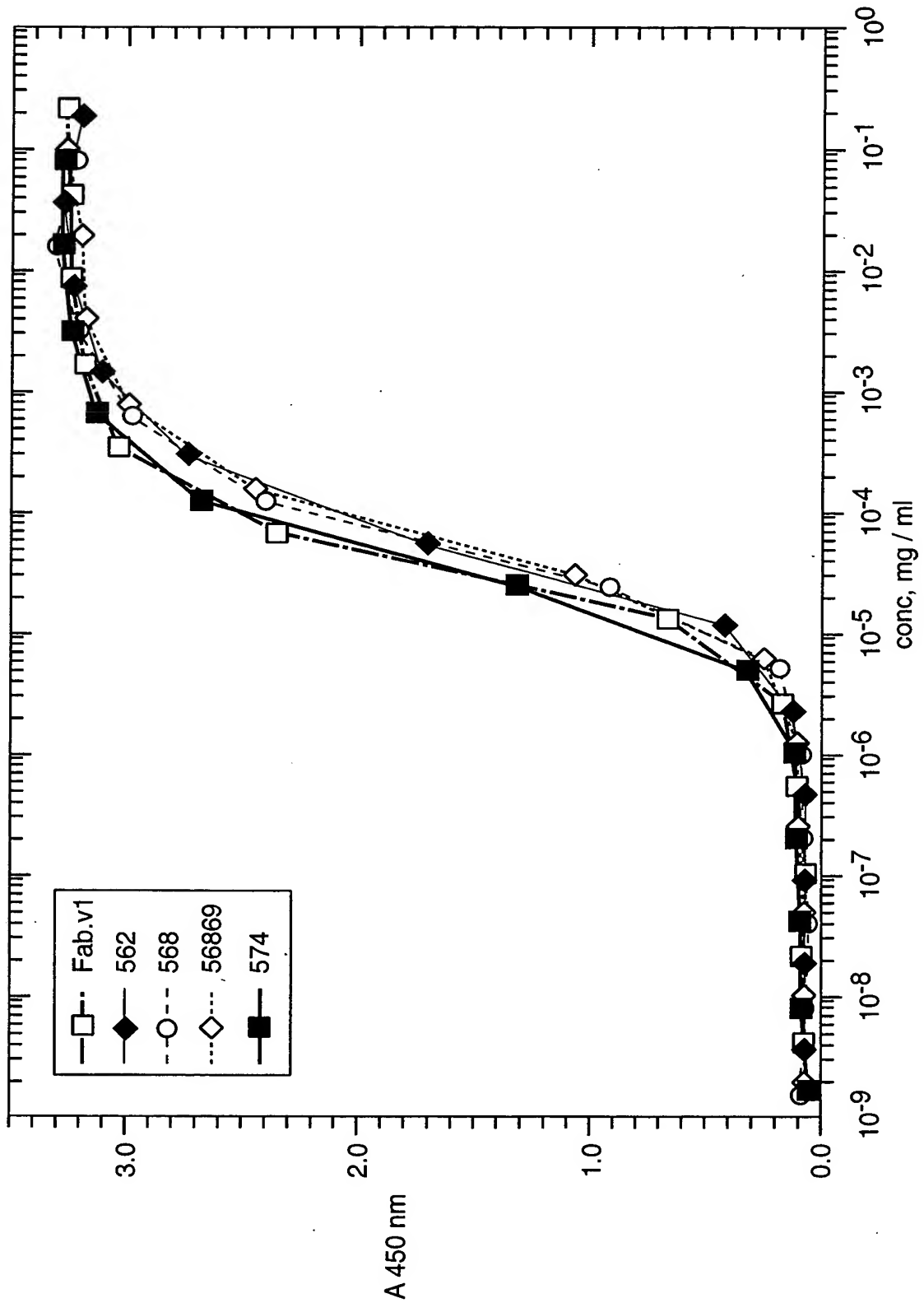


FIG._8C

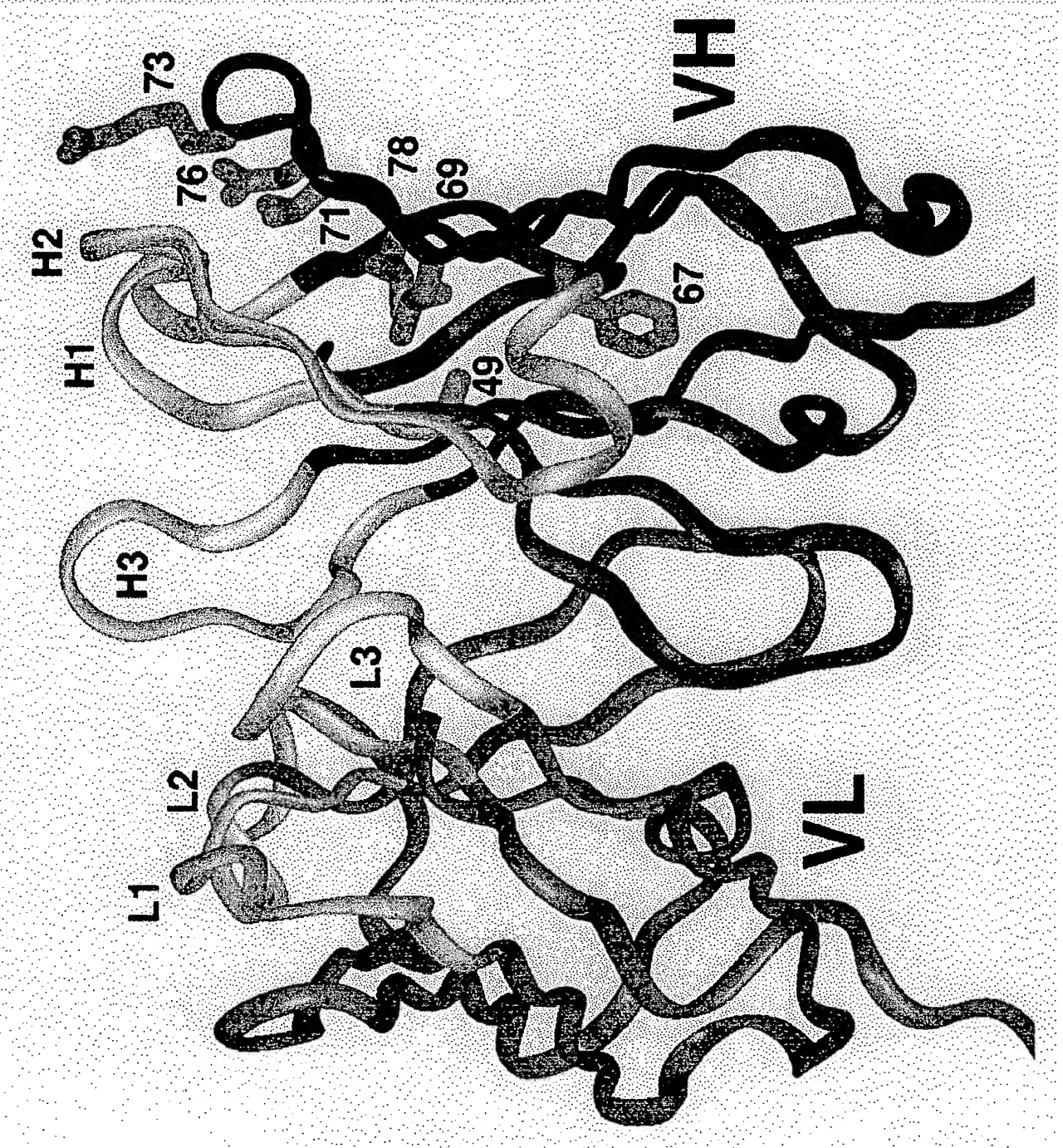


FIG. 9